Figure 1

1 pel B

MET LYS TYR LEU LEU PRO THR ALA ALA ALA GLY LEU

AAGCTTGCATGCAAATTCTATTTCAAGGAGACAGTCATAA ATG AAA TAC CTA TTG CCT ACG GCA GCC GCT GGA TTG

TTCGAACGTACGTTTAAGATAAAGTTCCTCTGTCAGTATT TAC TTT ATG GAT AAC GGA TGC CGT CGG CGA CCT AAC

Hin dIII

77 *Sfi* I *Pst* I *Not* I

*LEU LEU LEU ALA ALA GLN PRO ALA MET ALA GLU VAL GLN LEU GLN *** *** ALA ALA ALA*

TTA TTA CTC GCG GCC CAG CCG GCC ATG GCC GAG GTG CAA CTG CAG TAA TAG GCG GCC GCA

AAT AAT GAG CGC CGG GTC GGC CGG TAC CGG GTC CAC GTC GAC GTC ATT ATC CGC CGG CGT

137

GLY GLY GLY GLY SER MET GLU SER ALA LYS GLU THR ARG TYR CYS ALA VAL CYS ASN ASP

GGG GGA GGA GGG TCC ATG GAA TCT GCC AAG GAG ACT CGC TAC TGT GCA GTG TGC AAT GAC

CCC CCT CCT CCC AGG TAC CTT AGA CGG TTC CTC TGA GCG ATG ACA CGT CAC ACG TTA CTG

197

TYR ALA SER GLY TYR HIS TYR GLY VAL TRP SER CYS GLU GLY CYS LYS ALA PHE PHE LYS

TAT GCT TCA GGC TAC CAT TAT GGA GTC TGG TCC TGT GAG GGC TGC AAG GCC TTC TTC AAG

ATA CGA AGT CCG ATG GTA ATA CCT CAG ACC AGG ACA CTC CCG ACG TTC CGG AAG AAG TTC

257

ARG SER ILE GLN GLY HIS ASN ASP TYR MET CYS PRO ALA THR ASN GLN CYS THR ILE ASP

AGA AGT ATT CAA GGA CAT AAC GAC TAT ATG TGT CCA GCC ACC AAC CAG TGC ACC ATT GAT

TCT TCA TAA GTT CCT GTA TTG CTG ATA TAC ACA GGT CGG TGG TTG GTC ACG TGG TAA CTA

317 Oestrogen receptor DBD

LYS ASN ARG ARG LYS SER CYS GLN ALA CYS ARG LEU ARG LYS CYS TYR GLU VAL GLY MET

AAA AAC AGG AGG AAG AGC TGC CAG GCC TGC CGG CTC CGT AAA TGC TAC GAA GTG GGA ATG

TTT TTG TCC TCC TTC TCG ACG GTC CGG ACG GCC GAG GCA TTT ACG ATG CTT CAC CCT TAC

377

MET LYS GLY GLY ILE ARG LYS ASP ARG ARG GLY GLY ARG MET LEU LYS HIS LYS ARG GLN

ATG AAA GGT GGG ATA CGA AAA GAC CGA AGA GGA GGG AGA ATG TTG AAA CAC AAG CGC CAG

TAC TTT CCA CCC TAT GCT TTT CTG GCT TCT CCT CCC TCT TAC AAC TTT GTG TTC GCG GTC

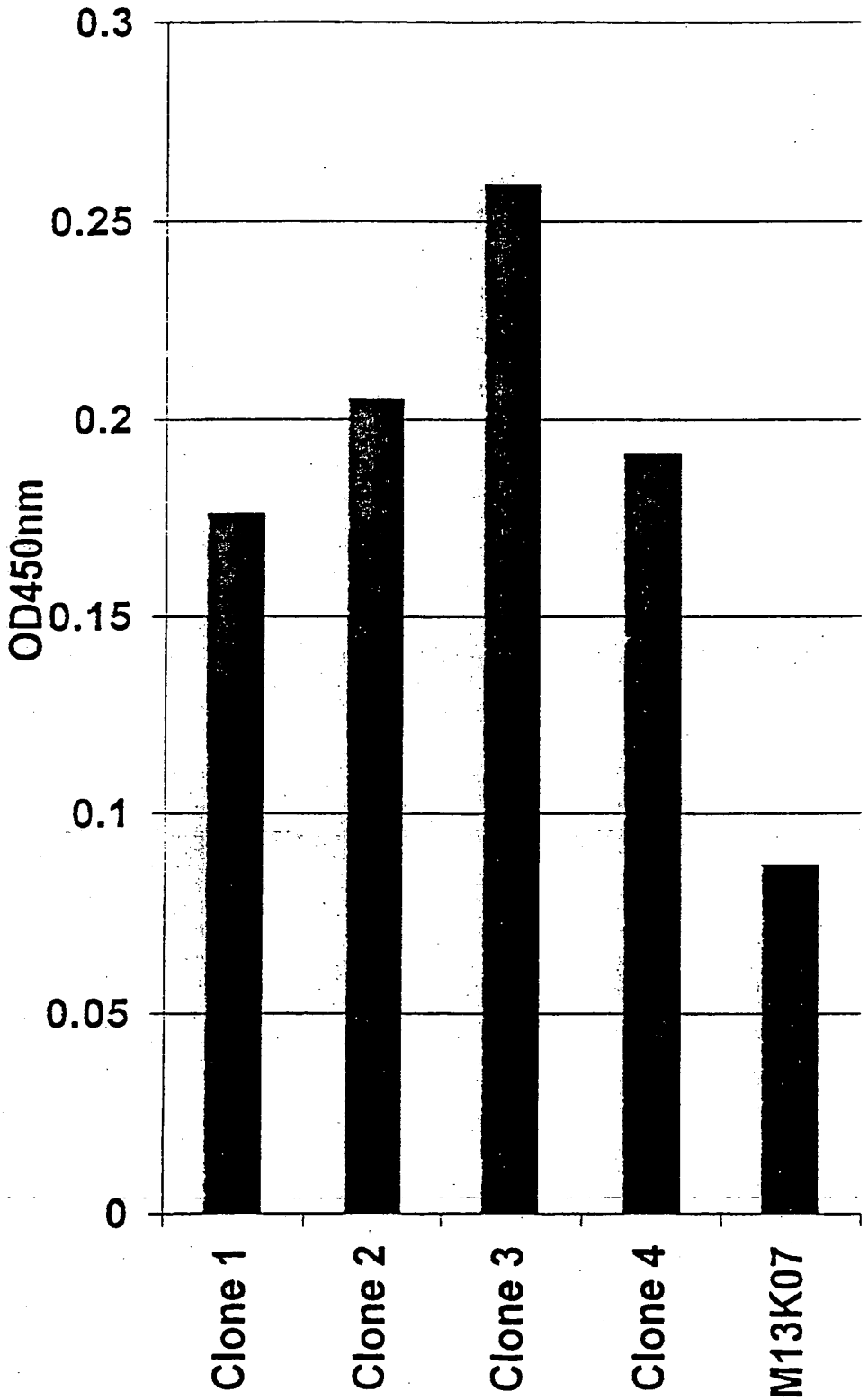
437

ARG ASP ASP GLY GLU GLY ARG GLY GLU VAL GLY SER *** *** HRE *Eco* RI

AGA GAT GAT GGG GAG GGC AGG GGT GAA GTG GGG TCT TGA TAA TCAGGTCAGAGTGACCTGAGCTAAAATAACACATTCAG AATTC

TCT CTA CTA CCC CTC CCG TCC CCA CTT CAC CCC AGA ACT ATT AGTCCAGTCTCACTGGACTCGATTTTATTGTGTAAGTC TTAAG

Figure 2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0.25
0.2
0.15
0.1
0.05
0
OD450nm
Clone 1
Clone 2
Clone 3
Clone 4
M13K07

Figure 3

Human Igk constant region

K R T V A A P S V

AAACGAACTGTGGCTGCACCATCTGTC

Clone #2

M A↓Q P T T R P G Q G T R L D I K R T V A A P S V

ATGGCCCAGCCCACCACGCGTCCGGGCCAAGGGACACGACTGGACATTAAACGAACTGTGGCTGCACCATCTGTC

Clone #3

M A↓Q S H H A S G G G T K V E I K R T V A A P S V

ATGGCCCAGTCCCACCACGCGTCCGGCGGAGGGACCAAGGTGGAGATCAAACGAACTGTGGCTGCACCATCTGTC

Human Igk constant region

F I F P P S D E Q L K S G T A S V V C L L N N F Y

TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTAT

Clone #2

F I F P P S D E Q L K S G T A S V V C L L N N F Y

TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTAT

Clone #3

F I F P P S D E Q L K S G T A S V V C L L N N F Y

TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTAT

Figure 4

4/9 pel B

1*Hin* dIII *MET LYS TYR LEU LEU PRO THR ALA ALA*

AAGCTTGCAT GCAAATTCTA TTTCAAGGAG ACAGTCATAA ATG AAA TAC CTA TTG CCT ACG GCA GCC

TTCGAACGTA CGTTTAAGAT AAAGTTCCTC TGTCAGTATT TAC TTT ATG GAT AAC GGA TGC CGT CGG

68 *Sfi* I *Pst* I

ALA GLY LEU LEU LEU LEU ALA ALA GLN PRO ALA MET ALA GLU VAL GLN LEU GLN *** ***

GCT GGA TTG TTA TTA CTC GCG GCC CAG CCG GCC ATG GCC GAG GTG CAA CTG CAG TAA TAG

CGA CCT AAC AAT AAT GAG CGC CGG GTC GGC CGG TAC CGG CTC CAC GTT GAC GTC ATT ATC

128 *Not* I

ALA ALA ALA GLY GLY GLY GLY SER MET GLU SER ALA LYS GLU THR ARG TYR CYS ALA VAL

GCG GCC GCA GGG GGA GGA GGG TCC ATG GAA TCT GCC AAG GAG ACT CGC TAC TGT GCA GTG

CGC CGG CGT CCC CCT CCT CCC AGG TAC CTT AGA CGG TTC CTC TGA GCG ATG ACA CGT CAC

188

CYS ASN ASP TYR ALA SER GLY TYR HIS TYR GLY VAL TRP SER CYS GLU GLY CYS LYS ALA

TGC AAT GAC TAT GCT TCA GGC TAC CAT TAT GGA GTC TGG TCC TGT GAG GGC TGC AAG GCC

ACG TTA CTG ATA CGA AGT CCG ATG GTA ATA CCT CAG ACC AGG ACA CTC CCG ACG TTC CGG

248

PHE PHE LYS ARG SER ILE GLN GLY HIS ASN ASP TYR MET CYS PRO ALA THR ASN GLN CYS

TTC TTC AAG AGA AGT ATT CAA GGA CAT AAC GAC TAT ATG TGT CCA GCC ACC AAC CAG TGC

AAG AAG TTC TCT TCA TAA GTT CCT GTA TTG CTG ATA TAC ACA GGT CGG TGG TTG GTC ACG

308

THR ILE ASP LYS ASN ARG ARG LYS SER CYS GLN ALA CYS ARG LEU ARG LYS CYS TYR GLU

ACC ATT GAT AAA AAC AGG AGG AAG AGC TGC CAG GCC TGC CGG CTC CGT AAA TGC TAC GAA

TGG TAA CTA TTT TTG TCC TCC TTC TCG ACG GTC CGG ACG GCC GAG GCA TTT ACG ATG CTT

368

VAL GLY MET MET LYS GLY GLY ILE ARG LYS ASP ARG ARG GLY GLY ARG MET LEU LYS HIS

GTG GGA ATG ATG AAA GGT GGG ATA CGA AAA GAC CGA AGA GGA GGG AGA ATG TTG AAA CAC

CAC CCT TAC TAC TTT CCA CCC TAT GCT TTT CTG GCT TCT CCT CCC TCT TAC AAC TTT GTG

428

LYS ARG GLN ARG ASP ASP GLY GLU GLY ARG GLY GLU VAL GLY SER Ter Ter HRE 1

AAG CGC CAG AGA GAT GAT GGG GAG GGC AGG GGT GAA GTG GGG TCT TGA TAA TCAGGTCAGAGT

TTC GCG GTC TCT CTA CTA CCC CTC CCG TCC CCA CTT CAC CCC AGA ACT ATT AGTCCAGTCTCA

491 HRE 1 *Sal* I HRE 2 *Eco* RI

GACCTGAGCTAAAATAACACATTCAG GTCGAC TTGGGTCAGTCTGACCGGGACAAAGTTAATGTAACCTC GAATTC

CTGGACTCGATTTTATTGTGTAAGTC CAGCTG AACCCAGTCAGACTGGCCCTGTTTCAATTACATTGGAG CTTAAG

Figure 5

pel B

1 *Hin*DIII *MET LYS TYR LEU LEU PRO THR ALA ALA*

AAGCTTGCAT GCAAATTCTA TTTCAAGGAG ACAGTCATAA ATG AAA TAC CTA TTG CCT ACG GCA GCC

TTCGAACGTA CGTTTAAGAT AAAGTTCCTC TGTCAGTATT TAC TTT ATG GAT AAC GGA TGC CGT CGG

68

ALA GLY LEU LEU LEU LEU ALA ALA GLN PRO ALA MET ALA GLU MET GLU SER ALA LYS GLU

GCT GGA TTG TTA TTA CTC GCG GCC CAG CCG GCA ATG GCC GAG ATG GAA TCT GCC AAG GAG

CGA CCT AAC AAT AAT GAG CGC CGG GTC GGC CGT TAC CGG CTC TAC CTT AGA CGG TTC CTC

128

THR ARG TYR CYS ALA VAL CYS ASN ASP TYR ALA SER GLY TYR HIS TYR GLY VAL TRP SER

ACT CGC TAC TGT GCA GTG TGC AAT GAC TAT GCT TCA GGC TAC CAT TAT GGA GTC TGG TCC

TGA GCG ATG ACA CGT CAC ACG TTA CTG ATA CGA AGT CCG ATG GTA ATA CCT CAG ACC AGG

188

CYS GLU GLY CYS LYS ALA PHE PHE LYS ARG SER ILE GLN GLY HIS ASN ASP TYR MET CYS

TGT GAG GGC TGC AAG GCC TTC TTC AAG AGA AGT ATT CAA GGA CAT AAC GAC TAT ATG TGT

ACA CTC CCG ACG TTC CGG AAG AAG TTC TCT TCA TAA GTT CCT GTA TTG CTG ATA TAC ACA

248

PRO ALA THR ASN GLN CYS THR ILE ASP LYS ASN ARG ARG LYS SER CYS GLN ALA CYS ARG

CCA GCC ACC AAC CAG TGC ACC ATT GAT AAA AAC AGG AGG AAG AGC TGC CAG GCC TGC CGG

GGT CGG TGG TTG GTC ACG TGG TAA CTA TTT TTG TCC TCC TTC TCG ACG GTC CGG ACG GCC

308

LEU ARG LYS CYS TYR GLU VAL GLY MET MET LYS GLY GLY ILE ARG LYS ASP ARG ARG GLY

CTC CGT AAA TGC TAC GAA GTG GGA ATG ATG AAA GGT GGG ATA CGA AAA GAC CGA AGA GGA

GAG GCA TTT ACG ATG CTT CAC CCT TAC TAC TTT CCA CCC TAT GCT TTT CTG GCT TCT CCT

368

GLY ARG MET LEU LYS HIS LYS ARG GLN ARG ASP ASP GLY GLU GLY ARG GLY GLU VAL GLY

GGG AGA ATG TTG AAA CAC AAG CGC CAG AGA GAT GAT GGG GAG GGC AGG GGT GAA GTG GGG

CCC TCT TAC AAC TTT GTG TTC GCG GTC TCT CTA CTA CCC CTC CCG TCC CCA CTT CAC CCC

428 *Sfi* I *Pst* I *Not* I

SER GLY GLY GLY GLY SER ALA GLN PRO ALA LEU LEU GLN LEU ALA ALA ALA TER

TCT GGG GGA GGA GGG TCG GCC CAG CCG GCC CTC CTG CAG CTG GCG GCC GCA TAACTGATTG

AGA CCC CCT CCT CCC AGC CGG GTC GGC CGG GAG GAC GTC GAC CGC CGG CGT ATTGACTAAC

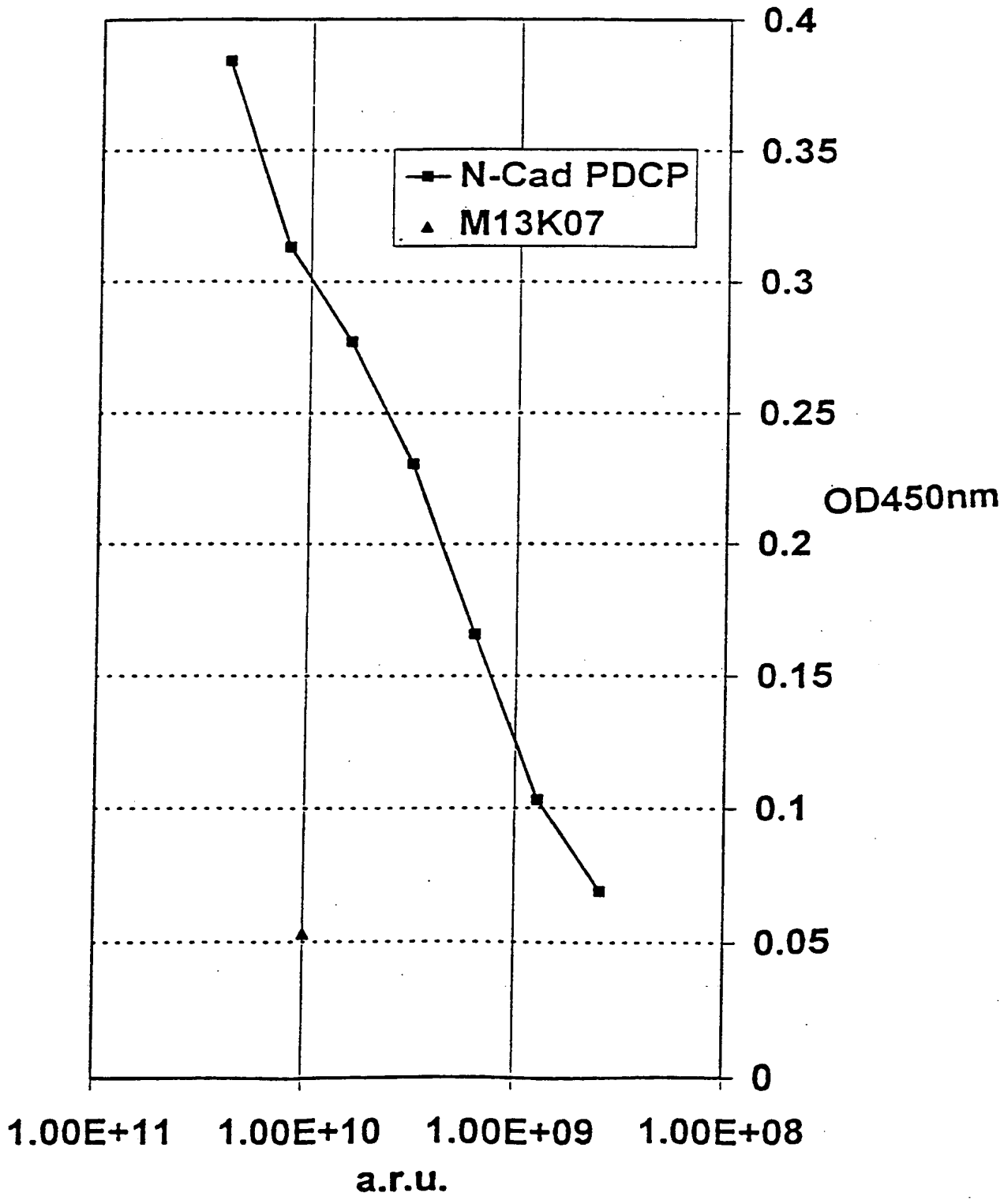
489 *Sal* I *Eco* RI

AGTCGACTTG GGTCAGTCTG ACCGGGACAA AGTTAATGTA ACCTC GAATTC

TCAGCTGAAC CCAGTCAGAC TGGCCCTGTT TCAATTACAT TGGAG CTTAAG

HRE

Figure 6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0.3
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0.15
0.1
0.05
0
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N-Cad PDCP
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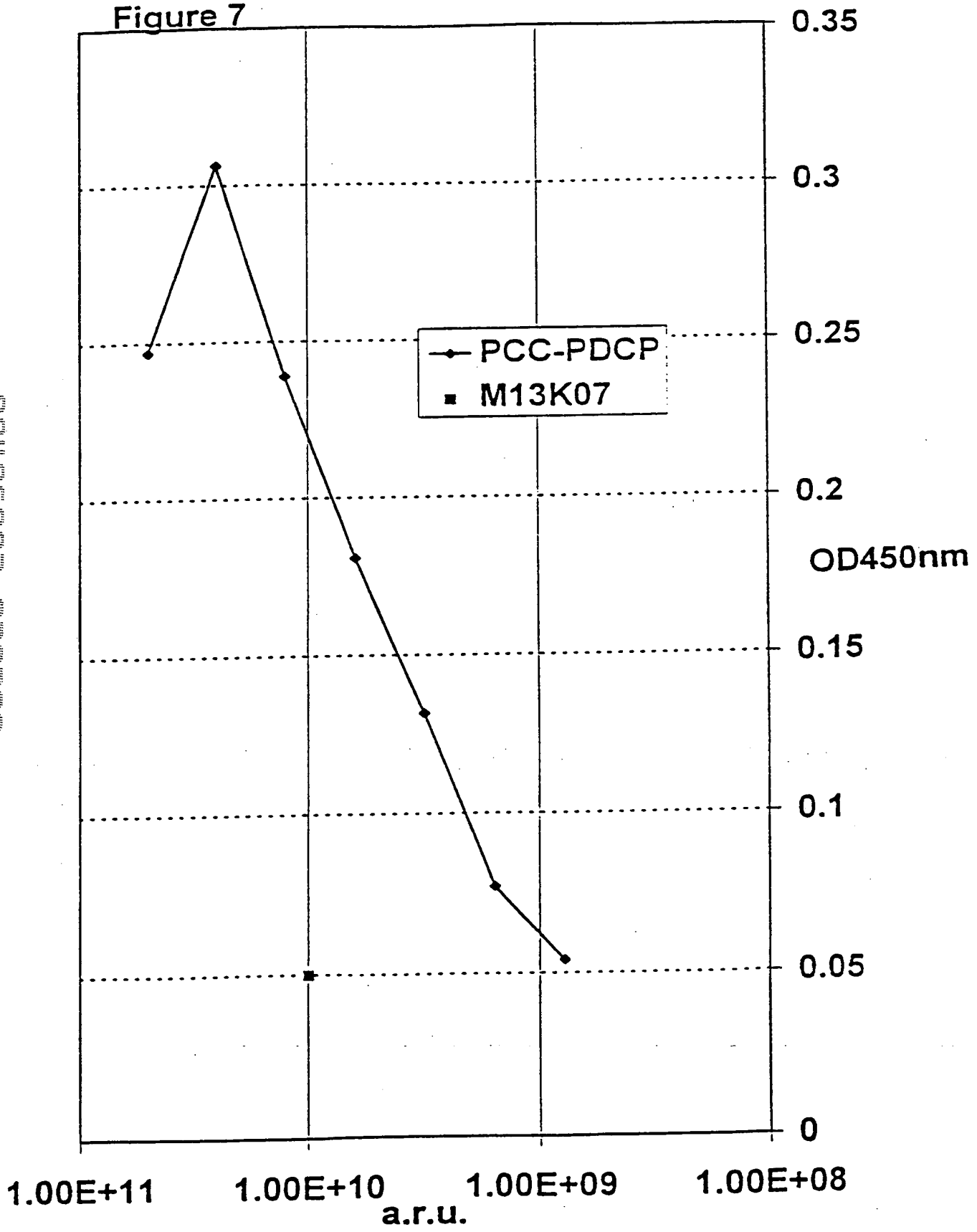
1.00E+11
1.00E+10
1.00E+09
1.00E+08
a.r.u.

Figure 7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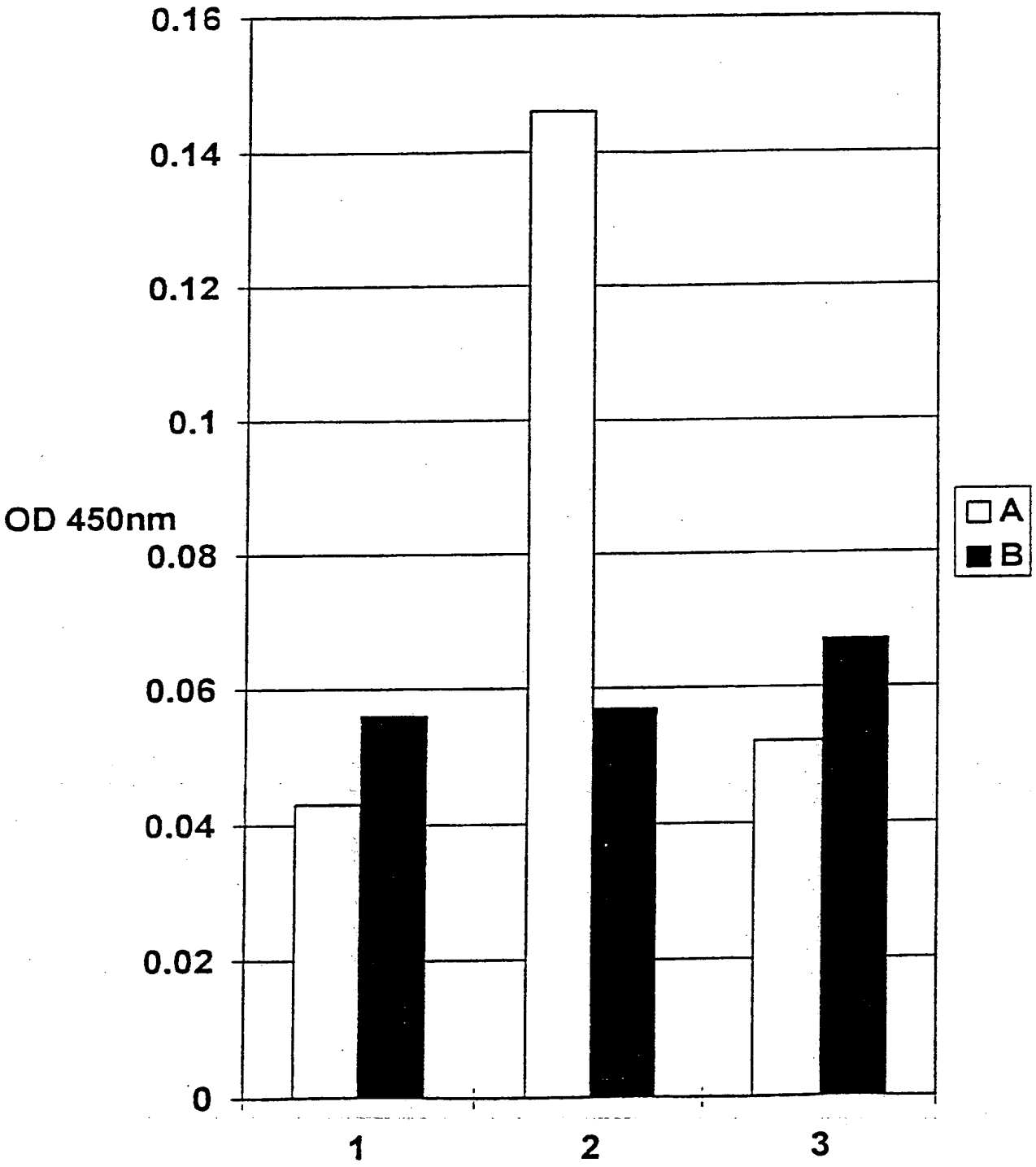
a.r.u.

Figure 8



HEAVY CHAIN 9/9 **Figure 9**

```
Q  V  Q  L  Q  Q  S  G  G  G  V  V  Q  P  G  R  S  L
CAGGTACAGCTGCAGCAGTCAGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTG
GTCCATGTCGACGTCGTCAGTCCCCCTCCGCACCAGGTCGGACCCTCCAGGGAC

R  L  S  C  A  A  S  G  F  P  F  S  T  Y  G  M  H  W
AGACTCTCCTGTGCAGCCTCGGGATTCCCCTTTAGTACTTATGGCATGCACTGG
TCTGAGAGGACACGTCGGAGCCCTAAGGGGAAATCATGAATACCGTACGTGACC

R  Q  A  V  P  G  K  G  L  E  W  V  A  V  I  S  Y  D
CGCCAGGCTGTCCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGAT
GCGGTCCGACAGGGTCCGTTCCCCGACCTCACCCACCGTCAATATAGTATACTA

G  S  N  K  Y  Y  A  D  S  V  K  G  R  F  T  I  S  R
GGAAGTAATAAATACTACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGA
CCTTCATTATTTATGATGCGTCTGAGGCACTTCCCGGCTAAGTGGTAGAGGTCT

D  N  S  K  N  T  L  Y  L  Q  M  N  S  L  R  A  E  D
GACAATTCCAAGAACACGTTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGAC
CTGTTAAGGTTCTTGTGCAACATAGACGTTTACTTGTCGGACTCTCGACTCCTG

T  A  V  Y  Y  C  A  R  D  L  D  P  T  R  Y  S  S  G
ACGGCTGTGTATTACTGTGCGAGAGATTTAGACCCCACCAGGTATAGCAGTGGC
TGCCGACACATAATGACACGCTCTCTAAATCTGGGGTGGTCCATATCGTCACCG

W  D  T  D  Y  W  G  Q  G  H  L  V  T  V  S  S
TGGGACACTGACTACTGGGGCCAGGGGCACCTGGTCACTGTCTCCTCA
ACCCTGTGACTGATGACCCCGGTCCCCGTGGACCAGTGACAGAGGAGT
```

LIGHT CHAIN

```
E  T  T  L  T  Q  S  P  G  T  L  S  L  S  P  G  E  R
GAAACGACACTCACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCGGGGGAAAGA
CTTTGCTGTGAGTGCGTCAGAGGTCCGTGGGACAGAAACAGAGGCCCCCTTTCT

A  T  L  S  C  R  A  S  Q  N  I  G  S  S  S  L  A  W
GCCACCCTCTCCTGCAGGGCCAGTCAGAATATTGGCAGCAGCTCCTTAGCCTGG
CGGTGGGAGAGGACGTCCCGGTCAGTCTTATAACCGTCGTCGAGGAATCGGACC

Y  Q  Q  K  P  G  Q  A  P  R  L  L  I  Y  G  A  S  T
TACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACC
ATGGTTGTCTTTGGACCGGTCCGAGGGTCCGAGGAGTAGATACCACGTAGGTGG

R  A  T  G  F  S  G  S  G  S  G  T  Q  F  T  L  T  I
AGGGCCACTGGTTTCAGTGGCAGTGGGTCAGGGACACAATTCACTCTCACCATC
TCCCGGTGACCAAAGTCACCGTCACCCAGTCCCTGTGTTAAGTGAGAGTGGTAG

I  P  A  R  S  S  L  Q  S  E  D  F  A  V  Y  Y  C  Q
ATCCCAGCCAGGAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAG
TAGGGTCGGTCCTCGTCGGACGTCAGACTTCTAAAACGTCAAATAATGACAGTC

Q  Y  N  F  W  P  F  T  F  G  P  G  T  K  L  E  I  K
CAGTATAATTTCTGGCCATTCACTTTTGGCCCTGGGACCAAGCTGGAGATCAAA
GTCATATTAAAGACCGGTAAGTGAAAACCGGGACCCTGGTTCGACCTCTAGTTT

R
CGT
GCA
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